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Studies on carcass quality traits in two populations of Coho salmon (*Oncorhynchus kisutch*): phenotypic and genetic parameters

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Abstract

Phenotypic and genetic parameter estimates of carcass quality traits were obtained from two pedigreed populations, termed even and odd, of a Coho salmon breeding program. Carcass quality data from 3444 fish (1802 male and 1642 female), harvested at 21 months of age, were analyzed. In both populations, significant sex effects were found for body weight (3487–3354 g, male and female, respectively), total visceral weight (448–397 g), gonad weight (239–166 g), abdominal fat percentage (8.9–10%), fillet percentage (56.5–59.3%), total width of steak (8.2–8.0 cm), area of cutlet (231–217 cm^3), but not for abdominal fat weight (40.8–40.8 g), total fillet weight (2284–2263 g), texture of flesh (1.47–1.46 Kg) and fat content of flesh (18.0–18.1%). Less consistent significant sex effects were found for carcass weight (3086–2944 g, odd population), dressing percentage (86.9–88.8, even population), dorsal fat thickness (1.77–1.71 cm, odd), ventral thickness (1.14–1.17 cm, even) and height of cutlet (5.0–4.7 cm, odd).

Heritability estimated for carcass quality traits was medium in magnitude for total visceral weight (0.19–0.33, even and odd), gonad weight (0.26–0.33), abdominal fat weight (0.24–0.35), abdominal fat percentage (0.18–0.26), dressing percentage (0.33–0.23), while estimated heritability was low to

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medium for body weight (0.13–0.24), carcass weight (0.12–0.22), total fillet weight (0.18, odd), fillet percentage (0.11, odd), dorsal fat thickness (0.09–0.15), ventral thickness (0.05–0.22), total width of steak (0.10–0.30), height of cutlet (0.09–0.24), area of cutlet (0.11–0.33), texture of flesh (0.06–0.09) and fat content of flesh (0.17, even).

Estimated genetic correlations (r_g) between various biometrical traits of fish were all positive and ranged from 0.48 to 0.96, while the phenotypic correlations ranged from 0.33 to 0.90. Selection for increased body weight (growth) will produce favourable changes in carcass weight (r_g=0.99), fillet percentage (0.98), and texture (0.30–0.70), but unfavourable changes in dressing percentage (−0.48 to −0.03) and fat content of flesh (0.73). Estimates of genetic correlation were positive and moderate between abdominal fat percentage and fat content of flesh (0.46), and were negative between abdominal fat percentage and carcass weight (−0.45), and between abdominal fat percentage and dressing percentage (−0.44 to −0.11).

Keywords: Heritability; Salmon culture; Flesh quality traits; Fillet; Chile

1. Introduction

Body composition and carcass quality traits, including meat color, fat content and texture of flesh, directly influence yield of final product and consumer preference. In this sense, the most important breeding programs developed for salmonid species have incorporated, after a few generations of selection for growth rate, some quality traits as selection criteria (Gjedrem, 2000). Several genetics studies on body and carcass traits linked to these breeding programs have been performed in Atlantic salmon (Gjerde and Gjedrem, 1984; Rye and Refstie, 1995; Rye and Gjerde, 1996) and rainbow trout (Gjerde and Gjedrem, 1984; Gjerde and Schaeffer, 1989), in order to establish sampling and measuring techniques and to estimate the magnitude of phenotypic and the additive genetic variances and covariance between traits. However, the genetic information available for these types of traits in Coho salmon (*Oncorhynchus kisutch*) is limited (Iwamoto et al., 1990; Whithler and Beacham, 1994). Whithler and Beacham (1994) estimated heritability values for flesh color of adult fish close to 0.2, while Iwamoto et al. (1990) showed that the level of lipid and whole weight have heritabilities of around 0.19 and 0.35, respectively, with a positive genetic correlation between them (approximately 0.30).

Chilean salmonid production reached 332,000 tons in 2002 (SERNAPESCA, 2003) and Coho salmon production represents close to a third of it. The first Coho salmon breeding program in Chile began in 1992 (Neira, 1997), after which several breeding programs were started in private companies (Dunham et al., 2001; Neira, 2002). Several of these programs have included growth rate and some compositional or carcass traits as selection criterion (Neira, 2002).

The aim of the present study was to estimate phenotypic and genetic parameters for body weight and carcass quality traits in Coho salmon, using data of fish harvested from the Coyhaique Coho salmon breeding program.

2. Materials and methods

2.1. Coho populations and data set

The study was based on data from two Coho salmon populations from the genetic improvement center (CMG) maintained by the Institute for Fisheries Development (IFOP) and the University of Chile in Coyhaique (XI Region, Chile). The two populations termed 'even' and 'odd' were produced in 1992 and 1993, respectively, and are managed in a 2-year reproductive cycle. Since initiation of the program, the two populations have been managed as closed populations and maintained by spawning 30–35 males with 100 females each season. The fish were spawned between April and June, hatched and reared in separate full-sib family tanks until marking in December to establish the pedigree. At this age fish were transferred to estuary water conditions (Ensenada Baja) and smoltification occurred 8 months after spawning. Harvest took place in February at 20–21 months of age. Artificial selection was practised for high harvest weight and spawn date of females. More details on characters and origins of the populations have been given by Martínez et al. (1999), Winkler et al. (1999), Gall and Neira (2004) and Gallardo et al. (2004).

Fish used for this study were freeze branded as alevins, and represented a random sample of about 80 individuals as replicates from the selected families of the breeding program (all spawned within a range of 15–20 days of the spawning season); the fish were marked in December at a mean weight of 8.73 g (S.D.=2.58) and 8.66 g (S.D.=3.22) in odd and even population, respectively, and stocked into rearing cages in the sea. Families were equally distributed among cages if more than one cage was used and the cages placed in the estuary (Ensenada Baja) where the fish remained until harvest (1996=one cage; 1997=two cages; 1998=10 cages; 1999=four cages). During this period, the fish were all fed with commercial pellet according to fish requirement by weight.

Data on carcass quality from 3444 fishes were obtained from year-classes 1996–1998 and 1997–1999 (Table 1), representing the second and third generations of selection from the even and odd population.

2.2. Recorded traits

Slaughter occurred from February 1st to 12th each year, after an average 10-day starvation period. Fish anaesthetised with high CO_2 were bled by cutting the gill arches and the recording of data on quality traits started after 12 h in containers under ice.

Table 1
Data structure

Year-class	Year of harvest	Number of offspring	Number of sires	Number of dams
1996	1998	615	26	86
1997	1999	1006	30	100
1998	2000	982	31	99
1999	2001	842	31	96
Total		3444	118	381

The following traits were recorded. Biometrical traits: body weight (BW) to the nearest 50 g; body fork length (BL) to the nearest 0.1 cm; body width (BWd), to the nearest 0.1 cm measured at widest part; body height (BH), to the nearest 0.1 cm measured at the deepest part. Traits measured in the steak, a cross-sectional cut obtained by cutting between just posterior to the base of the pectoral fins and the base of the dorsal fin (Gjerde (1989): left width (LWd), right width (RWd), ventral thickness (VT) and dorsal fat thickness (DF) and height of cutlet (HC), all measured to the nearest 0.1 cm, as shown in Fig. 1. Area of cutlet (AC) was defined as half the area of the ellipse with rays HC and (1/2)(RWd+LWd). Visceral traits, measured to the nearest gram: total viscera weight (TVW), gonad weight (GW) and abdominal fat weight (AFW), determined by weighting dissected intestinal fat. The following derived variables were also calculated: carcass weight (CW)=BW−TVW; dressing percentage (D%)=(CW×100)/BW; condition factor (K)=(BW(g)×100)/(BL(cm))^3; gonadosomatic index (GI)=GW×100)/BW; abdominal fat percentage (AF%)=(AFW×100)/TVW. Fillet percentage (Fl%) was calculated as (TFW×100)/BW where TFW is the total weight of fillets obtained by a trained person. Flesh quality traits were measured in the steak: fat content of flesh (F%) and flesh texture (TX). Fat content of flesh was measured by liquid chromatography (HPLC; Weber, 1990) on 1996 fish and by Near Infrared Spectrophotometry (NIR; Solberg, 1992) on 1998 fish. Flesh texture was determined only in 1998 and 1999 by using a fruit pressure penetrometer (mod. FT-011, Facchini, Italy). The whole carcass, with the fillet exposed (the skin removed), was placed on a firm base under the penetrometer. The plunger (11-mm

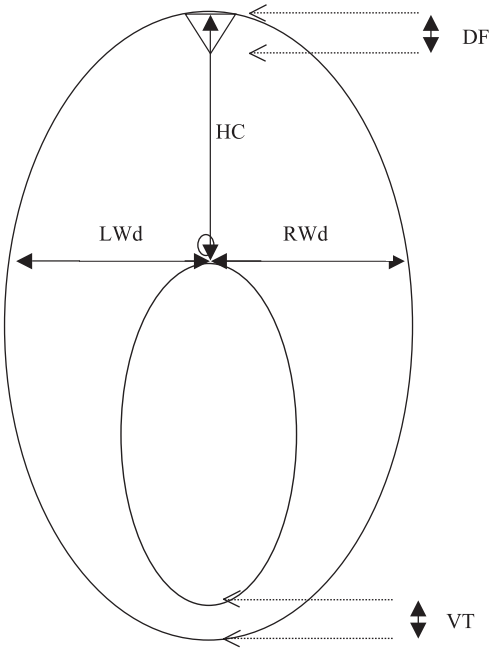

Fig. 1. Cross-sectional cut performed posterior to the dorsal fins, to measure: left width (LWd), right width (RWd), ventral thickness (VT) and dorsal fat thickness (DF), height of cutlet (HC).

diameter) penetrated to a constant depth (2 cm) in the left side fillet halfway above the lateral line just anterior to the dorsal fin (location 2 sensu Sigurgisladottir et al., 1999). The pressure recorded was at the breaking point (kg) of the flesh and was taken as a measure of toughness.

2.3. Statistical analyses

Analyses of variance (GLM procedure of SAS, 1996) were performed to evaluate the following fixed effects in all traits for each population separately: year-class, sex, cage and interaction sex by cage. Also, Least Square Means ware estimated for all carcass traits in even and odd populations. Percent values were arcsine transformed to approximate normal distribution, which was confirmed using Kolmogorov–Smirnov test for Normality (Zar, 1984).

Animal models were constructed for each year-class and population. Univariate and bivariate analyses were carried out using a Restricted Maximum Likelihood (REML) algorithm through the ASREML program (Gilmour et al., 1999) for obtaining the (co)variance components. Heritabilities and correlations were calculated from these estimates. The general model used in matrix notation was:

$$\boldsymbol{y} = \mathbf{X}\boldsymbol{b} + \mathbf{Z}\boldsymbol{a} + \mathbf{Z}\boldsymbol{e} \tag{1}$$

where $\boldsymbol{y}$ is a vector of observations, $\boldsymbol{b}$ is a vector of fixed effects (the same fixed effects were considered for each phenotype in bivariate analyses), $\boldsymbol{a}$ is a vector of random additive genetic values, $\boldsymbol{e}$ is a vector of random residual effects. $\mathbf{X}$ is a known design matrix relating $\boldsymbol{y}$ with fixed effects and $\mathbf{Z}$ is a known matrix relating $\boldsymbol{y}$ with additive genetic values and residual effects, respectively. Significant fixed effects detected in the analyses of variance were included in the model. Only animal was included as a random effect.

The expectation and variance–covariance matrix associated with the Eq. (1) is assumed to be:

Univariate analyses

$$E\begin{bmatrix} b \\ a \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \end{bmatrix}; \ \mathrm{Var}[a_1] = [Ag_{ii}] \text{ and } \mathrm{Var}[e_1] = [Ir_{ii}],$$

Bivariate analyses

$$E\begin{bmatrix} b \\ a \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \end{bmatrix}; \ \mathrm{Var}\begin{bmatrix} a_i \\ a_j \end{bmatrix} = \begin{bmatrix} Ag_{ii} & Ag_{ij} \\ Ag_{ij} & Ag_{jj} \end{bmatrix} \text{ and } \mathrm{Var}\begin{bmatrix} e_i \\ e_j \end{bmatrix} = \begin{bmatrix} Ir_{ii} & Ir_{ij} \\ Ir_{ij} & Ir_{jj} \end{bmatrix},$$

where A is the numerator of relationships matrix among animals of these two generations. I is the identity matrix, $g_{ii}=\sigma^2_{ai}$ and $g_{jj}=\sigma^2_{aj}$ are the variances of additive genetic effects for i and j trait, $r_{ii}=\sigma^2_{ei}$ and $r_{jj}=\sigma^2_{ej}$ are the variance of residuals effects, and $g_{ij}=\sigma^2_{aij}$ and $r_{ij}=\sigma^2_{eij}$ are the covariance of additive genetic effects and residual effects for i and j trait.

3. Results

3.1. Phenotypic means and variation

Phenotypic means, standard deviations and coefficients of variation for biometrical, visceral, steak and flesh traits are given in Table 2. The year-class 1996 and 1999 showed the highest values for all the biometrical traits analyzed. Further, these year-classes showed the highest total visceral weight, gonad weight, and abdominal fat weight; however, the dressing percentage and the gonadosomatic index were similar among the four year-classes and abdominal fat percentage was highest in the odd population. Higher

Table 2
Phenotypic means, standard deviations (S.D.) and coefficients of variation (CV) within year-class for carcass traits

Trait	1996			1997			1998			1999		
	Mean	S.D.	CV	Mean	S.D.	CV	Mean	S.D.	CV	Mean	S.D.	CV
Age at harvest (days)	637			640			628			633		
Biometrical												
Body weight (BW)	3914	659	16.8	3010	662	21.9	3337	817	24.5	3925	834	21.3
Body length (BL)	61.4	3.2	5.2	57.3	4.4	7.7	58.1	5.0	8.1	60.1	4.2	7.0
Condition factor (*K*)	1.7	0.1	8.7	1.6	0.2	10.0	1.7	0.2	11.1	1.8	0.2	12.7
Body height (BH)	16.2	1.2	7.6	15.3	1.6	10.1	16.0	1.7	10.6	16.9	1.6	9.3
Body width (BWd)	7.4	0.9	11.6	7.2	1.0	14.4	7.5	0.8	10.3	8.3	0.9	11.2
Visceral												
Total visceral weight (TVW)	500	130	26.1	343	92.3	26.9	388	113	29.1	558	143	25.7
Gonad weight (GW)	258	91	35.2	161	62	38.3	190	83	44.0	267	97	36.4
Abdominal fat weight (AFW)	40.3	21.1	52.3	32.6	16.5	50.6	29.7	16.5	55.7	69.0	30.4	43.9
Abdominal fat percentage (AF%)	7.9	3.2	40.0	9.7	4.6	48.0	7.7	4.2	53.9	12.5	5.1	40.9
Carcass weight (CW)	3435	568	16.5	2667	588	22.1	2950	721	24.4	3367	718	21.3
Dressing percentage (D%)	86.9	2.0	2.4	88.6	1.9	2.2	87.9	1.9	2.2	85.8	2.1	2.4
Gonadosomatic index (GI)	6.5	1.8	28.3	5.3	1.8	33.2	5.6	2.0	35.7	6.8	2.0	29.0
Total fillet weight (TFW)	–	–	–	–	–	–	–	–	–	2274	512	22.5
Fillet percentage (Fl %)	–	–	–	–	–	–	–	–	–	57.8	3.8	6.5
Steak												
Dorsal fat thickness (DF)	1.3	0.2	13.0	1.7	0.3	16.2	1.3	0.2	17.4	–	–	–
Ventral fat thickness (VT)	1.2	0.2	15.0	1.0	0.2	19.3	1.2	0.2	19.3	1.6	0.3	16.1
Total width (TWd)	8.2	0.6	6.7	8.4	0.9	10.3	7.7	0.8	10.2	–	–	–
Height of cutlet (HC)	–	–	–	4.9	0.6	11.9	3.7	0.4	11.9	–	–	–
Area of cutlet	–	–	–	263.5	51.3	19.5	184.3	36.8	19.9	–	–	–
Flesh												
Texture (TX)	–	–	–	–	–	–	1.7	0.3	17.9	1.2	0.2	20.6
Fat content (F%)	20.6	3.5	17.2	–	–	–	17.8	2.0	11.0	–	–	–

phenotypic variation was observed for the visceral traits than biometrical traits (Table 2). For biometrical traits the coefficient of variation was approximately 10% except for body weight at harvest (17–25%). In contrast, the coefficient of variation for visceral traits varied between 16% and 52%. Phenotypic means for steak traits were similar between populations, but the phenotypic variation observed was highest in year-classes 1997 and 1998 (Table 2).

3.2. Sex effects

Least square means and standard errors of carcass traits for sex within population are presented in Table 3. In general, males showed significantly ($P<0.05$) higher mean values

Table 3
Least mean square in carcass traits for male (M) and female (F), and differences between male–female (%) per population

Trait	Even population			Odd population		
	M	F	M−F %	M	F	M−F (%)
Biometrical						
Body weight (BW)	3423±32	3330±33	2.7*	3551±24	3378±25	5.1**
Body length (BL)	58.3±0.17	58.4±0.18	0.2	58.9±0.14	58.4±0.14	0.9*
Condition factor (*K*)	1.68±0.01	1.64±0.01	2.4**	1.70±0.01	1.66±0.01	2.4**
Body height (BH)	16.2±0.06	15.9±0.07	1.9**	16.3±0.05	15.9±0.05	2.8**
Body width (BWd)	7.5±0.03	7.4±0.04	1.3	7.8±0.03	7.7±0.03	1.7**
Visceral						
Total visceral weight (TVW)	430±4.8	59±4.9	19.8**	465±3.8	435±3.9	6.9**
Gonad weight (GW)	240±3.0	46±3.1	64.2**	239±2.3	187±2.3	27.8**
Abdominal fat weight (AFW)	30.1±0.9	31.3±0.8	−3.9	51.5±0.8	50.3±0.8	2.3
Carcass weight (CW)	2995±29	2973±30	0.7	3086±21.2	2944±21.8	4.8**
Dressing percentage (D%)	86.9±0.08	88.8±0.08	−2.1**	87.2±0.06	87.3±0.06	−0.1
Gonadosomatic index (GI)	7.0±0.06	4.2±0.06	64.8**	6.6±0.05	5.5±0.05	20.0**
Abdominal fat percentage (AF%)	6.8±0.17	8.7±0.17	−22.3**	10.9±0.16	11.3±0.17	−3.5**
Total fillet weight (TFW)	–	–	–	2284±24.3	2263±25.2	0.9
Fillet percentage (Fl%)	–	–	–	56.5±0.2	59.3±0.2	−4.7**
Steak						
Dorsal fat thickness (DF)	1.28±0.01	1.29±0.01	0.7	1.77±0.01	1.71±0.01	3.5**
Ventral fat thickness (VT)	1.14±0.01	1.17±0.01	−2.6**	1.29±0.01	1.29±0.01	0
Right width (RWd)	3.83±0.02	3.77±0.02	1.6*	4.28 ±0.02	4.17±0.02	2.6**
Left width (LWd)	3.95±0.02	3.90±0.02	1.3*	4.27±0.02	4.16±0.02	2.6**
Total width (TWd)	7.77±0.03	7.66±0.03	1.4*	8.55±0.04	8.34±0.04	2.5**
Height of cutlet (HC)	3.74±0.02	3.69±0.02	1.3	5.03±0.03	4.73±0.03	6.3**
Area of cutlet (AC)	187±1.70	181±1.80	2.8*	274±2.3	252±2.3	8.7**
Flesh						
Texture (TX)	1.74±0.01	1.72±0.02	1.1	1.19±0.01	1.19±0.01	0
Fat content (F%)	18.0±0.12	18.1±0.13	0.2	–	–	–

* $P<0.05$.
** $P<0.001$.

than females in all biometrical traits in both populations, where male–female differences varied from 1% to 5%. Most of visceral traits showed very significant sex differences ($P<0.001$) in both populations; however, the magnitude of the male–female (M−F) differences were generally greater in the even than in the odd population for total visceral weight (19.8–6.9%, respectively), gonad weight (64–27%), dressing percentage (2.1–0.1%), gonadosomatic index (65–20%) and abdominal fat percentage (22–3.5%). Males have higher mean values in visceral traits than females, except in dressing percentage (M−F=−2.1%, even population), abdominal fat percentage (−22% and −3.5%, even and odd population) and fillet percentage (−4.7%, odd population). No significant sex effects ($P>0.05$) were observed for abdominal fat weight and total fillet weight.

Sex differences were generally significant on steak traits (male higher than female) but not on flesh traits (Table 3). Furthermore, for the visceral traits the magnitude of the male–female differences was greater and highly significant ($P<0.001$) in the even population than in the odd population. Fillet texture and fat content of flesh showed no significant differences between sexes ($P>0.05$) in either population.

Table 4
Estimated heritabilities (h^2) and standard error (S.E.) for carcass traits

	Even year-class	1996	1998	Odd year-class	1997	1999
	h^2 S.E.	h^2	h^2	h^2 S.E.	h^2	h^2
Biometrical						
Body weight (BW)	0.13±0.04	0.30	0.09	0.24±0.05	0.30	0.17
Body length (BL)	0.17±0.05	0.28	0.16	0.20±0.05	0.23	0.13
Condition factor (K)	0.21±0.05	0.30	0.18	0.24±0.05	0.32	0.18
Body height (BH)	0.07±0.03	0.23	0.04	0.18±0.05	0.20	0.15
Body with (BWd)	0.07±0.03	0.14	0.08	0.09±0.03	0.29	0.03
Visceral						
Total visceral weight (TVW)	0.19±0.06	0.29	0.09	0.33±0.06	0.38	0.27
Gonad weight (GW)	0.26±0.06	0.35	0.15	0.33±0.06	0.35	0.25
Abdominal fat weight (AFW)	0.24±0.06	0.31	0.11	0.35±0.06	0.41	0.36
Abdominal fat percentage (AF%)	0.18±0.06	0.36	0.10	0.26±0.05	0.29	0.26
Carcass weight (CW)	0.12±0.04	0.27	0.10	0.22±0.05	0.28	0.15
Dressing percentage (D%)	0.33±0.07	0.31	0.28	0.23±0.05	0.31	0.19
Gonadosomatic index (GI)	0.35±0.07	0.35	0.28	0.31±0.06	0.34	0.19
Total fillet weight (TFW)	–	–	–	0.18±0.07	–	0.18
Fillet percentage (Fl%)	–	–	–	0.11±0.05	–	0.11
Steak						
Dorsal fat thickness (DF)	0.09±0.04	0.08	0.09	0.15±0.06	0.15	–
Ventral fat thickness (VT)	0.05±0.03	0.25	0.00	0.22±0.05	0.24	0.19
Total width (TWd)	0.10±0.04	0.14	–	0.30±0.07	0.30	–
Height of cutlet (HC)	0.09±0.05	–	0.09	0.24±0.07	0.24	–
Area of cutlet (AC)	0.11±0.05	–	0.11	0.33±0.07	0.33	–
Flesh						
Texture (TX)	0.06±0.04	–	0.06	0.09±0.04	0.06	0.09
Fat content (F%)	0.17±0.06	0.26	0.00	–	–	–

3.3. Heritabilities

Estimates of heritabilities were different between populations and year-classes but showed similar standard errors of low magnitude (Table 4). Heritabilities of the first generations analyzed (1996 and 1997) were higher than those of the last generations (1998 and 1999), indicating a possible combination management differences with a selection and sampling effect in the estimates, which will be discussed below. Estimates of heritabilities in the odd population were higher than those in even population for all traits except for dressing percentage and gonadosomatic index. In both populations, estimates of heritability for biometrical traits were low to medium in magnitude (0.07–0.24), while the estimates for visceral traits were generally medium (0.20–0.35) with low heritabilities for carcass weight (0.12–0.22) and fillet percentage (0.11). Estimates of heritabilities for steak traits were low (0.05–0.11) in the even population but intermediate (0.15–0.33) in the odd population. Low heritabilities were obtained for fillet texture and fat content of flesh (0.06–0.17).

3.4. Correlations

Genetic and phenotypic correlations between biometrical traits and between some special interest traits, as those considering body weight, abdominal fat and fat content, are presented in Tables 5 and 6. All estimated correlations between biometrical traits were high and positive (>0.48) with the exception of some genetic correlations involving condition factor and body length (Table 5). Further, positive genetic correlations (>0.30) were found between body weight with carcass weight, fillet percentage, area of cutlet and fat content of flesh (Table 6). Body weight was also highly correlated with dorsal and ventral fat thickness (0.69–0.88) but only in the odd population, whereas genetic correlations were negative or close to zero between body weight and abdominal fat

Table 5
Phenotypic (above diagonal), genetic (below diagonal) correlations (×100) and standard errors (S.E.) of biometrical traits per population

	BW	BL	*K*	BWd	BH
Even population					
Body weight (BW)	–	89±01	48±02	90±01	86±01
Body length (BL)	81±07	–	07±03	81±01	79±01
Condition factor (*K*)	02±22 ns	−55±17	–	49±02	46±02
Body width (BWd)	88±06	48±19	33±23 ns	–	85±01
Body height (BH)	84±08	64±14	21±22 ns	80±11	–
Odd population					
Body weight (BW)	–	88±01	44±02	71±01	90±02
Body length (BL)	87±04	–	04±03 ns	66±02	80±01
Condition factor (*K*)	50±12	06±17 ns	–	33±02	48±02
Body width (BWd)	96±04	77±10	68±13	–	71±01
Body height (BH)	94±02	71±08	76±09	96±04	–

ns: not significantly different from zero ($P>0.05$).

Table 6
Genetic (r_g) and phenotypic (r_p) correlations (×100±S.E.) between body weight, abdominal fat % and percent fat with carcass traits within year-class

	Even population		Odd population	
	r_g	r_p	r_g	r_p
Body weight and:				
Carcass weight (CW)	98±01	99±01	99±01	99±01
Abdominal fat percentage (AF%)	−43±21	06±03	15±18 ns	06±04
Dressing percentage (%D)	−03±21 ns	−06±03	−48±14	−07±04
Fillet percentage (Fl %)	–	–	98±01	97±01
Dorsal fat thickness (DF)	11±27 ns	55±02	88±08	65±02
Ventral fat thickness (VT)	36±26 ns	63±02	69±10	55±03
Area of cutlet (AC)	95±05	86±01	97±02	88±01
Texture (TX)	30±39 ns	−01±04	70±19	22±03
Fat content (F%)	73±17	15±03	–	–
Abdominal fat percentage and:				
Carcass weight (CW)	−45±21	05±03	18±16 ns	−05±04
Dressing percentage (%D)	−44±17	−12±03	−11±16 ns	04±04
Dorsal fat thickness (DF)	−42±23 ns	03±03	32±21 ns	07±04
Ventral fat thickness (VT)	05±31 ns	12±03	24±16 ns	03±04
Area of cutlet (AC)	−35±28 ns	05±04	30±19 ns	−02±04
Texture (TX)	23±40 ns	01±04	02±28 ns	−06±04
Fat content (F%)	46±22	07±04	–	–
Fat content of flesh (F%) and:				
Carcass weight (CW)	73±01	17±03	–	–
Dressing percentage (%D)	−37±16	−10±04	–	–
Dorsal fat thickness (DF)	38±24 ns	12±03	–	–
Ventral fat thickness (VT)	50±28 ns	12±03	–	–
Area of cutlet (AC)	38±34 ns	17±05	–	–
Texture (TX)	70±37	02±05	–	–

ns: not significantly different from zero (P>0.05).

percentage (−0.43 and 0.15, even and odd population), and between body weight and dressing percentage (−0.30 and −0.48). Few genetic correlations were found significant between abdominal fat percentage and fat content of flesh with other quality traits. Abdominal fat percentage was positively correlated with fat content (0.46) and negatively correlated with carcass weight (−0.45) and dressing percentage (−0.44). Fat content showed a negative genetic correlation with dressing percentage (−0.37), but the opposite was found between this trait and carcass weight and texture, where a high positive genetic correlation was found (>0.70). Although an intermediate genetic correlation was found between fat content and ventral thickness (0.50), it was not significant.

Body weight showed a very low phenotypic correlation with abdominal fat percentage and with texture (Table 6). On the other hand, the phenotypic correlations between fat content of the flesh or abdominal fat percentage with other carcass traits tended to be smaller than the corresponding genetic correlations.

4. Discussion

This work is a genetic analysis on carcass traits in Coho salmon, with 3444 individuals from two populations and 21 traits analyzed. The different degrees of gonad development between sexes and the different rearing conditions between year-classes and populations produced a high variability among the genetic parameters obtained. Therefore, we first discuss those effects (sex and environment) before describing the significance and relevance of our results.

In almost all analyzed traits, except for some visceral traits, males showed significant higher values than females in both populations. Similar results have been published for Atlantic salmon (Rye and Gjerde, 1996) and rainbow trout (Gjerde 1989; Elvingson and Johansson, 1993). Most of these sexual differences are usually related with differences in fish size; however, Rye and Gjerde (1996) report that the status of sexual maturation substantially affects several body composition traits, usually with higher magnitude than sex effect. The Coho populations analyzed in this study showed clear carcass trait differences between sexes, which could be related to different degree of gonad development. Estay et al. (1998) reported for one of these populations (odd population) that males have a faster gonad growth than female during the early summer (January in Chile). Males have, in this period, a gonadosomatic index value (GI=3.9%) three times greater than females (1.4%); however, females begin an explosive gonad development after this point, a situation that continues until its GI value exceeds that of males at spawning time in May (8–17%, male–female). Our measurement of GI taken in February in both populations clearly follows Estay et al.'s (1998) description, but with higher gonadosomatic index values in both sexes (7.0–4.2% and 6.6–5.5%, even and odd, respectively). Therefore, they are consistent with the earlier gonad development of males, and with a different degree of maturation between sexes, as gonad development of females is farther than that of males to complete maturation at this stage. This is a very different situation from that described for Atlantic salmon (Rye and Gjerde, 1996) where the status of sexual maturation substantially affects several body composition traits, usually with higher magnitude than sex effect, because in these coho salmon populations, managed under a 2-year reproductive cycle, almost all fish are sexually mature and will spawn in May. Our results are more similar to those described for rainbow trout (Gjerde, 1989; Elvingson and Johansson, 1993) where most of these sexual differences are usually related with differences in fish size.

Heritabilities estimated separately for each generation were different in both populations, with those of the first generation (1996–1997) being higher than those estimated in the second generation (1998 and 1999). This apparent decrease in the heritability estimates across generations in biometrical and visceral traits must be discussed within population. Experimental design and management differences could explain the results in the even population. In 1998, random samples of fish from each family were placed in 10 cages, which were used in a nutrition experiment, while in 1996 only one cage was used. This major management difference between generations, which is connected with the higher coefficient of variation showed by most traits in 1998, could affect heritability estimates in this generation. The situation for the odd population cannot be connected with major management differences; therefore, the differences are more reasonably related with genetic sampling effects.

Heritability estimates by the animal model for harvest body weight (20–21 month of age) in Coho salmon were low to medium in magnitude (0.13–0.24). Similar estimated heritabilities have been reported by some works in rainbow trout (Gjerde and Gjedrem, 1984; Gjerde and Schaeffer, 1989). Higher estimates (0.35–0.43) have been published for rainbow trout (Elvingson and Johansson, 1993) and Atlantic salmon (Gjerde and Gjedrem, 1984). Additionally, our estimates of genetic correlations between biometrical traits were consistent with those published by other authors (Gjerde and Gjedrem, 1984; Rye and Refstie, 1995).

Dressing and fillet percentage are characteristics highly appreciated by fish processing companies. In this study, dressing percentage was close to 87% while fillet percentage was 58%. Medium heritability estimates were found (0.23–0.33) for dressing percentage, which is consistent with other studies in Atlantic salmon (Rye and Gjerde, 1996) and rainbow trout (Gjerde and Schaeffer, 1989), but low heritability (0.11) was found for fillet percentage. An adverse negative genetic correlation (−0.48) was found between dressing percentage and body weight but highly favourable between fillet percentage and body weight (0.98).

Large quantities of intestinal fat are considered a waste product by fish breeding as it reduces carcass yield. In this study, abdominal fat weight represented 7% of total visceral weight (AF%). Rye and Gjerde (1996) reported values of (4–5%) for abdominal fat index (AFI), which express abdominal fat weight over total body weight, which is a much higher value compared with our study in coho, where abdominal fat weight represents only 1% of total body weight. Heritability estimates for AF% were medium in magnitude, and were positive genetically correlated with fat content of flesh (0.46) and negative genetically correlated with carcass weight (−0.45) and dressing percentage (−0.44). Similar results have been reported in Atlantic salmon by Rye and Gjerde (1996), but their estimate of AFI was negatively correlated with fat content of flesh. This opposite results may indicate that body fat deposition and relocation are different in this specie. However, several other points should be considered here; one is the much lower intestinal fat depot in cohos, in which the population has gone only three generations of selection for body weight at harvest and fat content has not been considered as selection criteria until this point. Low heritabilities were obtained for fat content of flesh (0.17). Similar results were obtained by Iwamoto et al. (1990) in Coho salmon, but higher heritabilities have been reported for fat content in Atlantic salmon (Rye and Gjerde, 1996) and in rainbow trout (Gjerde and Schaeffer, 1989). On the other hand, body weight showed a high positive genetic correlation with fat content of flesh (0.73); lower genetic correlation was reported in coho salmon (Iwamoto et al., 1990) and in Atlantic salmon (Rye and Gjerde, 1996). In contrast, Gjerde and Schaeffer (1989) reported negative low correlation between body weight and fat content (−0.19) in rainbow trout. Because this coho selection program is based on harvest body weight, an increase in fat content of flesh may be expected as a correlated response. However, this estimated genetic correlation is not an estimate of the correlation between growth rate (e.g., measured as the number of days to a given body weight) and fat content of flesh (recorded at the same given body weight). This latter correlation would allow us to properly predict the correlated response on fat content when selection is practised for increased growth rate.

In this study the phenotypic correlation between body weight and fat content of the flesh was lower (0.15) than the genetic correlation (0.74), which may be explained by a

low environmental correlation. The same could explain the consistently lower phenotypic correlation than the corresponding genetic correlations between abdominal fat percentage and other carcass traits. This was also observed for the correlations between fat percentage and other carcass traits, but this was measured only in the even population. The phenotypic correlations between abdominal fat (score) and other carcass traits in the study of Gjerde and Schaeffer (1989) were also lower than the genetic correlations, but was not the case for body weight and fat.

Heritabilities obtained for ventral and dorsal thickness were low to medium. Similar estimates have been reported for a related trait as belly thickness by Rye and Refstie (1995) in Atlantic salmon and by Elvingson and Johansson (1993) in rainbow trout. Genetic correlation between fat traits with ventral thickness was always positive (0.05–0.50) although not significant. Positive relationship has also been reported by Gjerde and Schaeffer (1989) in rainbow trout between belly thickness and fat content (0.24), while a high positive genetic correlation was reported by Rye and Gjerde (1996) in Atlantic salmon between average belly thickness and fat fillet percentage (0.73). However, other traits may be more appropriate as a correlated measurement of fat content; Rye and Gjerde (1996) have suggested to use dry matter content as an indicator of fat content due to the high genetic correlation (0.94) found between them in Atlantic salmon.

Texture is another important characteristic of flesh, which is appreciated by consumers and food companies. Texture of flesh is directly determined by the structural characteristic of muscle (Johnston et al., 2000), but also it is strongly influenced by the method of slaughter and for the procedure of processing (Johnston, 2001). There is some evidence that structural characteristics of muscle are under genetic control, as differences have been found between families, populations and species (Johnston, 2001). Our result showed no evidence of genetic control for texture, as estimated heritability was very low (0.06–0.09); similar result has been reported by Lhorente (2001) in Atlantic salmon. Then, applying direct selection for increase texture will be of no use, at least with this mechanic system of measure. However, the high genetic correlation with body weight (0.70) estimated in this study for Coho salmon and for Atlantic salmon (Lhorente, 2001) permits to predict that direct selection for body weight will increase texture of flesh; however, a medium optimum value may be desired.

Selection for body weight will produce favourable increase in carcass weight, fillet percentage and texture of flesh, but unfavourable changes in dressing percentage and in all measurements of fat, like dorsal and ventral fat thickness, and fat content of flesh. These results make clear that fat content of flesh should be included as selection objective when selection for body weight is performed, to reduce the level of fat in the muscle and to increase the dressing percentage.

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